

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:13:04 ; Search time 101.54 Seconds
(without alignments)
48.262 Million cell updates/sec

Title: US-09-052-089a-5

Perfect score: 286

Sequence: 1 RALCTICSDFFDHSRDVAAM.....IOSFETAPSRTPCQCRIOVG 51

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	78.7	433	2 T30807	TRAF interacting p
2	114	39.9	310	2 C84701	hypothetical prote
3	113	39.5	158	2 T13738	hypothetical prote
4	112	39.2	325	2 F86321	FEA14.12 protein -
5	103	36.0	344	2 T05064	hypothetical prote
6	102	35.7	324	2 E84918	hypothetical prote
7	101	35.3	274	2 T48286	hypothetical prote
8	100	35.0	224	2 E86321	hypothetical prote
9	99	34.6	524	2 F96572	hypothetical prote
10	98	34.3	383	2 A86315	protein F12M16.10
11	95.5	33.4	506	2 F85016	F2H15.19 protein -
12	95	33.2	351	2 F96597	probable RING zinc
13	94	32.9	137	2 T46904	hypothetical prote
14	93	32.5	551	2 S6685	hypothetical prote
15	92.5	32.3	408	2 T25524	probable membrane
16	92.5	32.2	624	2 S28418	hypothetical prote
17	92	32.2	489	2 T26069	probable zinc-bind
18	91.5	32.0	441	2 F71425	hypothetical prote
19	90.5	31.6	206	2 C85067	hypothetical prote
20	90	31.5	190	2 T51859	hypothetical prote
21	89	31.1	367	2 H96764	protein RING zinc
22	89	31.1	292	2 T06684	hypothetical prote
23	89	31.1	425	2 T25457	hypothetical prote
24	88.5	30.9	405	2 A28009	43k postsynaptic m
25	87.5	30.6	157	2 T13037	RING-H2 finger pro
26	87.5	30.6	157	2 T51841	RING-H2 finger pro
27	87.5	30.6	194	2 C85130	hypothetical prote
28	87.5	30.6	203	2 T48129	hypothetical prote
29	87.5	30.6	425	2 A84849	probable RING zinc

30	86.5	30.2	477	2 JE0343
31	86.5	30.2	609	2 A43906
32	86	30.1	407	2 G96835
33	86	30.1	1238	2 T15919
34	85.5	29.9	227	2 T00428
35	85.5	29.9	1610	2 T11681
36	85	29.7	204	2 G84530
37	85	29.7	343	2 H96703
38	85	29.7	362	2 G84526
39	84.5	29.5	225	2 T04066
40	84.5	29.5	236	2 T04065
41	84.5	29.5	324	2 T08729
42	84.5	29.5	412	2 S45064
43	84	29.4	513	2 TVH0RE
44	84	29.4	610	2 T22687
45	84	29.4	801	4 TVH0RE

ALIGNMENTS

RESULT 1

T30807 TRAF interacting protein - Fugu rubripes

C:Species: Fugu rubripes

C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000

C:Accession: T30807

R:Cottage, A.J.; Clark, M.; Hawker, K.; Umranta, Y.; Wheller, D.; Bishop, M.; Elgar, F.E.B. Lett. 443, 370-374, 1999

A:Title: Three receptor genes for plasmidogen related growth factors in the genome of

A:Reference number: Z20880; MUID:99148833

A:Accession: T30807

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-433 <COT>

A:Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1

C:Genetics:

A:Gene: TRIP

A:Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3

Query Match 78.7%; Score 225; DB 2; Length 433;

Best Local Similarity 76.0%; Pred. No. 8.7e-20;

Matches 38; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 RALCTICSDFFDHSRDVAAMDCGHTFHLQCTIQSFETAPSRTPCQCRIOV 50

Db 4 RALCTICSDFFDHSRDVAAMDCGHTFHLQCTIQSFETAPSRTPCQCRIOV 53

RESULT 2

C84701 hypothetical protein At2g29840 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84701

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,

euuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: C84701

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-310 <STO>

A:Cross-references: GB:AE002093; NID:g3582320; PIDN:AMC35217.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g29840

A:Map position: 2

Query Match 39.9%; Score 114; DB 2; Length 310;

Best Local Similarity 39.6%; Pred. No. 2e-06;
Matches 19; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

OY 3 LCTICSDPFHSDRVAAAMDCGHTFHLOCLIOSFETAPSRTPCQCRIOY 50
Db 260 MCSICLDFEFDGRSIVLPCGHEFDECAIKWFT--NHDCPLCKRKL 305

RESULT 3

113738 hypothetical protein 22E5.12 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13738

R:Murphy, L.; Harris, D.; Barrell, B.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: 217668

A:Accession: T13738

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <MUR>

A:Cross-references: EMBL:AL031765; NID:e1371523; PID:e1326038; PIDN:CABA1708.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0000667

A:Introns: 41/2

A:Note: EG:22E5.12

C:Superfamily: RING finger homology

F:4-54/Domain: RING finger homology <RRN>

Query Match 39.5%; Score 113; DB 2; Length 158;
Best Local Similarity 48.9%; Pred. No. 1.5e-06;
Matches 23; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

OY 3 LCTICSDPFHSDRVAAAMDCGHTFHLOCLIOSFETAPSRTPCQCRIOY 49
Db 7 ICTTICSEKRTSDNTQAGSCGHAFHEDCL--DHMKRSQRTCPICRSQ 51

RESULT 4

F6A14.12 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001

C:Accession: F66321

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: F66321

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-325 <STO>

A:Cross-references: GB:AE005172; NID:96730707; PIDN:AAF27102.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 39.2%; Score 112; DB 2; Length 325;
Best Local Similarity 37.5%; Pred. No. 3.7e-06;
Matches 18; Conservative 11; Mismatches 17; Indels 2; Gaps 1;

OY 3 LCTICSDPFHSDRVAAAMDCGHTFHLOCLIOSFETAPSRTPCQCRIOY 50
Db 276 VCTICLDFEFDGRSIVLPCGHEFDECAIKWFT--VRSHWCPLCKRKL 321

RESULT 5

T05064 hypothetical protein M3E9.170 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000

C:Accession: T05064

R:Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hohnsels, J.; Nemes, H.W.; Ma

submitted to the Protein Sequence Database, March 1999

A:Reference number: 215396

A:Accession: T05064

A:Molecule type: DNA

A:Residues: 1-344 <BEV>

A:Cross-references: EMBL:AL022223

A:Experimental source: cultivar Columbia; BAC clone M3E9

C:Genetics:

A:Map position: 4

A:Note: M3E9.170

C:Superfamily: RING finger homology

F:225-275/Domain: RING finger homology <RRN>

Query Match 36.0%; Score 103; DB 2; Length 344;
Best Local Similarity 38.3%; Pred. No. 4.0e-05;
Matches 18; Conservative 8; Mismatches 19; Indels 2; Gaps 1;

OY 4 CTICSDPFHSDRVAAAMDCGHTFHLOCLIOSFETAPSRTPCQCRIOY 50
Db 229 CSICLDFEFDGRSKAKKLCGHOFHDCIOSAFNMKGAMCPCMR 273

RESULT 6

E84918 hypothetical protein At2g47700 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: E84918

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.W.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: E84918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-324 <STO>

A:Cross-references: GB:AE002093; NID:93738284; PIDN:AAC63626.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g47700

A:Map position: 2

Query Match 35.7%; Score 102; DB 2; Length 324;
Best Local Similarity 41.3%; Pred. No. 6e-05;
Matches 19; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

OY 4 CTIC--SDFPDHSDRVAAAMDCGHTFHLOCLIOSFETAPSRTPCQCR 47
Db 38 CSICLDFEFDGRSKAKKLCGHOFHDCIOSAFNMKGAMCPCMR 83

RESULT 7

T48296 hypothetical protein F9G14.60 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000

C:Accession: T48296

R:Bevan, M.; Terry, N.; Adlles, W.; Buysmaet, C.; Dasseville, R.; De Clerck, R.;

ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, April 2000

A:Reference number: 224491

A:Accession: T48296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <BEV>
A:Cross-references: EMBL:AL162973
A:Experimental source: cultivar Columbia; BAC clone F9G14
C:Genetics:
A:Map position: 5
A:Note: F9G14.60
C:Superfamily: RING finger homology
F:201-251/Domain: RING finger homology <RRN>

Query Match 35.3%; Score 101; DB 2; Length 274;
Best Local Similarity 38.3%; Pred. No. 6.8e-05;
Matches 18; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVYAMDCGHTFHLCLOISFETAPSTPCQCRIOV 50
Db 205 CVICKEKSEGRDYCEMPCQHFHMKCILPWL--SKNKCPCFCRPL 249

RESULT 8
E86321
hypothetical protein F6A14.13 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: E86321
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: E86321
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <STO>
A:Cross-references: GB:AE005172; NID:96730708; PIDN:AAF27103.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 35.0%; Score 100; DB 2; Length 224;
Best Local Similarity 38.3%; Pred. No. 7.5e-05;
Matches 18; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVYAMDCGHTFHLCLOISFETAPSTPCQCRIOV 50
Db 175 CTICLEEFNDGKVTWLPFCGHEFDECVLTFET--NHDCPLCPKRL 219

RESULT 9
F96572
protein F12M16.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96572
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719
A:Accession: F96572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-524 <STO>
A:Cross-references: GB:AE005173; NID:97769853; PIDN:AAF69531.1; GSPDB:GN00141
C:Genetics:
A:Gene: F12M16.10
A:Map position: 1

Query Match 34.6%; Score 99; DB 2; Length 524;
Best Local Similarity 36.4%; Pred. No. 0.00021;
Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVYAMDCGHTFHLCLOISFETAPSTPCQCR 47
Db 472 CTICQSEFKNEKATATDCGHEHAECLEKWL--IVKNCPCICK 513

RESULT 10
F86315
F2H15.19 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C:Accession: A86315
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: A86315
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <STO>
A:Cross-references: GB:AE005172; NID:99665074; PIDN:AAF97276.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 34.3%; Score 98; DB 2; Length 383;
Best Local Similarity 34.1%; Pred. No. 0.00021;
Matches 15; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVYAMDCGHTFHLCLOISFETAPSTPCQCR 47
Db 335 CSTICDEYEREDEVGELNCGSHFVHCVKWL--SRKNACPVCK 376

RESULT 11
F85016
Probable RING zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: F85016
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: F85016
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <STO>
A:Cross-references: GB:NC_001268; NID:97267624; PIDN:CAB80936.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4G01270
A:Map position: 4

RESULT 16
S28418
probable zinc-binding protein - Iberian ribbed newt
C:Species: Pleurodeles waltlil (Iberian ribbed newt)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000
C:Accession: S28418; S29476
R:Beljini, M.; Lacroix, J.C.; Gall, J.G.
EMBO J. 12, 107-114, 1993
A:Title: A putative zinc-binding protein on lampbrush chromosome loops.
A:Reference number: S28418; MUID:93154311
A:Accession: S28418
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-624 <BEL>
A:Cross-references: EMBL:L04190
R:Beljini, M.; Lacroix, J.C.; Gall, J.G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29476
A:Accession: S29476
A:Molecule type: mRNA
A:Residues: 1-263, 'LK', 266-624 <BE2>
A:Cross-references: EMBL:L04190; NID:g213867; PID:g213868
C:Comment: This DNA-binding phosphoprotein is enriched in nuclei of adult brain cells and
C:Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F:158-207/Domain: RING finger homology <RNG>

Query Match 32.3%; Score 92.5; DB 2; Length 624;
Best Local Similarity 31.8%; Pred. No. 0.0015;
Matches 14; Conservative 13; Mismatches 14; Indels 3; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFHLCLOISFETAPSTPCQRIQV 47
Db 162 CPICRSIF--KEPVILCEGHNFCKHCIDKSWESNASAFSCECK 202

RESULT 17
T26069
hypothetical protein W02A11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T26069
R:White, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20147
A:Accession: T26069
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-489 <WIL>
A:Cross-references: EMBL:Z82062; PIDN:CAB04890.1; GSPDB:GN00019; CESP:W02A11.3
A:Experimental source: clone W02A11
C:Genetics:
A:Gene: CESP:W02A11.3
A:Map position: 1
A:Introns: 58/3; 129/3; 361/3; 444/3
C:Superfamily: RING finger homology
F:429-479/Domain: RING finger homology <RRN>

Query Match 32.2%; Score 92; DB 2; Length 489;
Best Local Similarity 27.7%; Pred. No. 0.0014;
Matches 13; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFHLCLOISFETAPSTPCQRIQV 50
Db 433 CTVCISFDESDSIQKCNHVFHECIYKWLDI--NKRCPWCREEI 477

RESULT 18
F71425
hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: columbia
C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 02-Sep-2000
C:Accession: F71425
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; G
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvea, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t
A:Reference number: A71400; MUID:98121113
A:Accession: F71425
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-441 <BEV>
A:Cross-references: GB:297340; NID:g2244950; PID:e326963; PID:g2244955
C:Genetics:
A:Map position: 4COP9-4G3845
C:Superfamily: RING finger homology
F:278-329/Domain: RING finger homology <RRN>

Query Match 32.0%; Score 91.5; DB 2; Length 441;
Best Local Similarity 37.5%; Pred. No. 0.0015;
Matches 18; Conservative 9; Mismatches 18; Indels 3; Gaps 2;

OY 4 CTIC-SDFDHSRDVAMDCGHTFHLCLOISFETAPSTPCQRIQV 50
Db 282 CSVCLSEKDNESGRVMPCKRHFVHCIDMWFHSHS--CPICRSQI 327

RESULT 19
C85067
hypothetical protein AT4G05350 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: C85067
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: C85067
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <STO>
A:Cross-references: GB:NC_001268; NID:g7267295; PIDN:CAB81077.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4G05350
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical RING finger protein F16J13.210; RING

Query Match 31.6%; Score 90.5; DB 2; Length 206;
Best Local Similarity 36.0%; Pred. No. 0.001;
Matches 18; Conservative 7; Mismatches 20; Indels 5; Gaps 2;

OY 4 CTICSDFF---DHSRDVAMDCGHTFHLCLOISFETAPSTPCQRIQV 50
Db 157 CSICLESIVSGPKPRDVTMTCSHFVHNGCLEWLKR--KNTCPICRTEI 204

RESULT 20
T51859
RING-H2 finger protein RHGla [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51859
R:Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.
FEBS Lett. 436, 283-7, 1998
A:Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the
A:Reference number: Z13771; MUID:98452956
A:Accession: T51859

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-190 <JEN>
 A:Cross-references: EMBL:AF079183; PIDN:AAC69857.1

Query Match 31.5%; Score 90; DB 2; Length 190;
 Best Local Similarity 29.5%; Pred. No. 0.0011;
 Matches 13; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

Y 4 CTICSDFFDHSRDVAMDCGHTFHLOCLIOSEFTAPSTPCPCR 47
 Db 136 CCVCEYTEGEDMCTLECGHFHSQCIEMWLK--QKNLCPTCK 177

RESULT 21

H96764
 Protein RING zinc finger protein F25P22.18 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96764
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Lin, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719

A:Accession: H96764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-367 <STO>
 A:Cross-references: GB:AE005173; NID:96692739; PIDN:AAF24845.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F25P22.18
 A:Map position: 1

Query Match 31.5%; Score 90; DB 2; Length 367;
 Best Local Similarity 34.1%; Pred. No. 0.0019;
 Matches 15; Conservative 8; Mismatches 19; Indels 2; Gaps 1;

Y 4 CTICSDFFDHSRDVAMDCGHTFHLOCLIOSEFTAPSTPCPCR 47
 Db 319 CIIODEYAEARDEVEGELRCGRFHIDCVNWL--VRKNSCPVCK 360

RESULT 22

T06684
 hypothetical protein T17F15.140 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
 C:Accession: T06684
 R:Queller, F.; Choinsne, N.; Robert, C.; Brotlier, P.; Wincker, P.; Catolico, L.; Artig
 submitted to the Protein Sequence Database, April 1999

A:Reference number: Z15793
 A:Accession: T06684
 A:Molecule type: DNA
 A:Residues: 1-292 <OUE>
 A:Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.140
 A:Experimental source: cultivar Columbia; BAC clone T17F15

C:Genetics:
 A:Gene: ATSP:T17F15.140
 A:Map position: 3
 A:Introns: 37/3; 68/3; 90/3; 143/3; 181/3
 C:Superfamily: RING zinc finger homology
 F:105-215/Domain: RING zinc finger homology <RRN>

Query Match 31.1%; Score 89; DB 2; Length 292;
 Best Local Similarity 34.0%; Pred. No. 0.0021;
 Matches 16; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

Y 4 CTICSDFFDHSRDVAMDCGHTFHLOCLIOSEFTAPSTPCPCR 50
 Db 169 CLICIEFHIGHEVGLPCAHNFHECIDQWRLT--NVKCPRCRSV 213

RESULT 23

T25457
 hypothetical protein B0432.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C:Accession: T25457
 R:Henkhaus, J.; Wohldmann, P.
 submitted to the EMBL data library, December 1996
 A:Description: The sequence of C. elegans cosmid B0432.
 A:Reference number: 220038
 A:Accession: T25457

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-425 <HEN>
 A:Cross-references: EMBL:U80836; PIDN:AB37893.1; GSPDB:GN00020; CESP:B0432.9
 A:Experimental source: strain Bristol N2; clone B0432
 C:Genetics:
 A:Gene: CESP:B0432.9
 A:Map position: 2
 A:Introns: 64/3; 99/3; 165/1; 267/3; 350/2; 386/2
 C:Superfamily: RING zinc finger homology
 F:188-238/Domain: RING zinc finger homology <RRN>

Query Match 31.1%; Score 89; DB 2; Length 425;
 Best Local Similarity 36.4%; Pred. No. 0.0029;
 Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

Y 4 CTICSDFFDHSRDVAMDCGHTFHLOCLIOSEFTAPSTPCPCR 47
 Db 192 CSTCFEDLKQNDKISATVCGIYHHCISQWIAT--KRQPCSR 233

RESULT 24

A28009
 43k postsynaptic membrane protein - Pacific electric ray

C:Species: Torpedo californica (Pacific electric ray)
 C:Date: 19-May-1989 #sequence_revision 12-Mar-1993 #text_change 01-Dec-2000
 C:Accession: A28009; B60088; I50550; I50551
 R:Garr, C.; McCourt, D.; Cohen, J.B.
 Biochemistry 26, 7090-7102, 1987

A:Title: The 43-kilodalton protein of Torpedo nicotinic postsynaptic membranes: purif
 A:Reference number: A28009; MUID:88107644

A:Accession: A28009
 A:Molecule type: protein
 A:Residues: 1-386; 'D', 388-403; 'T', 405 <CA2>
 R:Baldwin, T.J.; Theriot, J.A.; Yoshinara, C.M.; Burden, S.J.
 Development 104, 557-564, 1988
 A:Title: Regulation of transcript encoding the 43k subsynaptic protein during develop
 A:Reference number: A60088; MUID:90032364

A:Accession: B60088
 A:Status: nucleic acid sequence not shown: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 364-405 <BAL>

R:Fall, D.E.; Mudd, J.; Shah, V.; Garr, C.; Cohen, J.B.; Merlie, J.P.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6302-6306, 1987

A:Title: cDNAs for the postsynaptic 43-kDa protein of Torpedo electric organ encode t
 A:Reference number: I50550; MUID:87317641

A:Accession: I50550
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 'MGDOQTK', 1-354; 'Y', 356-382 <FRA>
 A:Cross-references: GB:J02952; NID:g213240; PIDN:AAA9282.1; PID:g213241
 A:Accession: I50551

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487
A:Accession: A84849
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-425 <STO>
A:Cross-references: GB:AE002093; NID:g1871181; PIDN:AAB63541.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g42030
A:Map position: 2

Query Match 30.6%; Score 87.5; DB 2; Length 425;
Best Local Similarity 34.0%; Pred. No. 0.0044;
Matches 16; Conservative 9; Mismatches 19; Indels 3; Gaps 1;

QY 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIOSFETAPSRPCRCRIQV 50
Db 141 CYICLDL---SKDPVNTGCHLYCMSCLYOMLYQVSEAKECPVCKGEV 184

RESULT 30
JE0343
terf protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jun-2000
C:Accession: JE0343
R:Ogawa, S.; Goto, W.; Orlino, A.; Hosoi, T.; Ouchi, Y.; Muramatsu, M.; Inoue, S.
Biochem. Biophys. Res. Commun. 251, 515-519, 1998
A:Title: Molecular cloning of a novel RING finger-B box-coiled coil (RBCC) protein, *terf*
A:Reference number: JE0343; MUID:99011410
A:Accession: JE0343
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-477 <OGA>
C:Superfamily: rfp transforming protein; RING finger homology
F:12-71/Domain: RING finger homology <RRN>

Query Match 30.2%; Score 86.5; DB 2; Length 477;
Best Local Similarity 32.1%; Pred. No. 0.0065;
Matches 18; Conservative 7; Mismatches 18; Indels 13; Gaps 2;

QY 2 ALCTICSDFFDHSRDVAAMDCGHTFHLQCLIOSFETAPSR-----TCPCR 47
Db 14 ATCTICLDYF---TDPVNTACGHNFCRCIOMSWKKGKGRKKQKSGSPCPCCR 66

RESULT 31
A43906
nuclear phosphoprotein knf7 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C:Accession: A43906; S27947
R:Reddy, B.A.; Kloc, M.; Eicklin, L.
Dev. Biol. 148, 107-116, 1991
A:Title: The cloning and characterization of a maternally expressed novel zinc finger nu
A:Reference number: A43906; MUID:92038424
A:Accession: A43906
A:Molecule type: mRNA
A:Residues: 1-609 <RED>
A:Cross-references: EMBL:M63705; NID:g214914; PID:g214915
A:Note: sequence extracted from NCBI backbone (NCBIN:64515, NCBI:P:64520)
C:Genetics:
A:Gene: knf7
C:Superfamily: Xenopus nuclear phosphoprotein knf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F:141-190/Domain: RING finger homology <RNG>

Query Match 30.2%; Score 86.5; DB 2; Length 609;
Best Local Similarity 34.1%; Pred. No. 0.0081;

Matches 15; Conservative 9; Mismatches 17; Indels 3; Gaps 1;
QY 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIOSFETAPSRPCRCR 47
Db 145 CPLICVELF---KDPVMAACGHNFCRCIDKAMEGQSSPACPCR 185

RESULT 32
G96835
probable RING zinc finger protein, 53384-54880 [imported] - *Arabidopsis thaliana*
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96835
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719
A:Accession: G96835
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <STO>
A:Cross-references: GB:AE005173; NID:g6751714; PIDN:AAF27696.1; GSPDB:GN00141
C:Genetics:
A:Gene: F516.15
A:Map position: 1

Query Match 30.1%; Score 86; DB 2; Length 407;
Best Local Similarity 32.0%; Pred. No. 0.0065;
Matches 16; Conservative 9; Mismatches 23; Indels 2; Gaps 1;

QY 2 ALCTICSDFFDHSRDVAAMDCGHTFHLQCLIOSFETAPSRPCRCRIQV 51
Db 353 ASCCTLTRYGDDDEQVRELPCSHVHDCVDMKLT--NATCPICKKEVG 400

RESULT 33
T15919
hypothetical protein EED8.9 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
C:Accession: T15919
R:Chisoe, S.
submitted to the EMBL Data Library, July 1995
A:Description: The sequence of C. elegans cosmid EED8.
A:Reference number: Z18428
A:Accession: T15919
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1238 <CHI>
A:Cross-references: EMBL:U23484; NID:g733597; PID:g733606; PIDN:AA46769.1; CESP:EED
A:Experimental source: strain Bristol N2
A:Gene: CESP:EED8.9
C:Genetics:
A:Insertions: 16/3; 60/3; 140/1; 192/3; 269/2; 402/2; 637/3; 717/3; 769/1; 855/3; 888/3;
C:Superfamily: RING finger homology
F:904-950/Domain: RING finger homology <RRN>

Query Match 30.1%; Score 86; DB 2; Length 1238;
Best Local Similarity 40.9%; Pred. No. 0.018;
Matches 18; Conservative 5; Mismatches 15; Indels 6; Gaps 2;

QY 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIOSFETAPSRPCRCR 47
Db 908 CAVCLERMDS--VLATICNHSFHARCL---EQWADNTPCVR 945


```
RESULT 34
T00428
hypothetical protein At2g47560 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T30B22.14
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
R:Accession: T00428; G84916
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc
submitted to the EMBL Data Library, October 1998
A:Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence.
A:Reference number: Z14149
A:Accession: T00428
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-227 <R0U>
A:Cross-references: EMBL:AC002535; NID:g2529657; PID:g2529671
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402:761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84916
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-227 <STO>
A:Cross-references: GB:AE002093; NID:g2529671; PIDN:AAC62854.1; GSPDB:GN00139
C:Genetics:
A:Gene: T30B22.14; At2g47560
A:Map position: 2
A:Superfamily: Arabidopsis hypothetical protein F19I3.22; RING finger homology
F:104-155/Domain: RING finger homology <RRN>

Query Match 29.9%; Score 85.5; DB 2; Length 227;
Best Local Similarity 35.4%; Pred. No. 0.0044;
Matches 17; Conservative 8; Mismatches 20; Indels 3; Gaps 2;

OY 4 CTTC-SDFDHSRDVAMDCGHTFLQCLIOSFETAPSRTPCPCRIOY 50
Db 108 CVCILSEFEDEGRLLPKCGSHFVDCIDPWFPS--RSTCPLCRAPV 153

RESULT 35
T11681
hypothetical protein SPBC21D10.09c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
R:Accession: T11681
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z17313
A:Accession: T11681
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1610 <SEE>
A:Cross-references: EMBL:AL031536; NID:e1319499; PID:e1319508
A:Experimental source: strain 972h(-)
C:Genetics:
A:Map position: IIR
A:Introns: 10/2
A>Note: SPBC21D10.09c
C:Superfamily: RING finger homology
F:1554-1609/Domain: RING finger homology <RRN>

Query Match 29.9%; Score 85.5; DB 2; Length 1610;
Best Local Similarity 36.2%; Pred. No. 0.026;
Matches 17; Conservative 5; Mismatches 22; Indels 3; Gaps 1;
```

```
OY 4 CTICSDFFDHSRDVAMDCG---HTFHLQCLIOSFETAPSRTPCPCR 47
Db 1558 CAICYSVLSVERTLPLNKRCGTCRRHKFASCLYKWKFKSSNSRCPICR 1604

RESULT 36
G84530
probable RING-H2 zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
R:Accession: G84530
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402:761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84530
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-204 <STO>
A:Cross-references: GB:AE002093; NID:g4335724; PIDN:AAD17402.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g15580
A:Map position: 2

Query Match 29.7%; Score 85; DB 2; Length 204;
Best Local Similarity 34.0%; Pred. No. 0.0046;
Matches 16; Conservative 6; Mismatches 23; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFHLQCLIOSFETAPSRTPCPCRIOY 50
Db 158 CAILDRFKKERTVLVHPCAIKRFHSICLPLWLDI--NVYCPYCRDI 202
```

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RESULT 37
H96703
probable RING zinc finger protein T23K23.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R:Accession: H96703
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408:816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96703
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-343 <STO>
A:Cross-references: GB:AE005173; NID:g6553889; PIDN:AAF16555.1; GSPDB:GN00141
C:Genetics:
A:Gene: T23K23.8
A:Map position: 1

Query Match 29.7%; Score 85; DB 2; Length 343;
Best Local Similarity 25.5%; Pred. No. 0.0074;
Matches 12; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFHLQCLIOSFETAPSRTPCPCRIOY 50
Db 292 CCICLSYEDGAEIVSLPCNHHFHSITCYKWLKM--NATCPLCKFNT 336

RESULT 38
```

C84526
 hypothetical protein At2g15260 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G64526
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffitt, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: AB4420, MUID:20083487
 A:Accession: G64526
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-362 <STO>
 A:Cross-references: GB:AE002093; NID:g4662636; PID:AAD26908.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g15260
 A:Map position: 2

Query Match	29.7%	Score 85;	DB 2;	Length 362;
Best Local Similarity	32.7%	Pred. No. 0.0077;		
Matches	16;	Conservative	6;	Mismatches 22; Indels 4; Gaps 1;
Oy	3	ICTGSDPF----	DHSRYAAMDCHHTHTLQCLIOSFETAPSRTPQPCR	47
Db	122	LCISIRGALVNMENDVORTLVTLCKCYHKKHRLDITGSATINAKNGMEPCNCR	170	

RESULT 39
T04066
Hypochemical protein F28M11.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 02-Sep-2000
C:Accession: T04066
R:Bayan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15184
A:Accession: T04066
A:Molecule type: DNA
A:Residues: 1-225 <BEV>
A:Cross-references: EMBL:AL049487
A:Experimental source: cultivar Columbia; BAC clone F28M11
C:Genetics:
A:Map position: 4
A:Introns: 68/3: 96/2
A:Note: F28M11.80
C:Superfamily: RING finger homology
P:93-144/Domain: RING finger homology <RRN>

	Query Match	Score	DB 2,	length	225;
Best Local Similarity	31.2%	Pred. No. 0.0058			
Matches	15;	Conservative	9;	Mismatches	21;
				Indels	3;
				Gaps	2;
QY	4	CTICSDFFDHSRDVAM-DCGHTFHLOCTIOSFEAPSTCQCRIQV	50		
Db	97	CSVCAGDVAQEERKLOMPSCGHTFMECI-DLWLTSHATCTCRSL	142		

```

RESULT 40
T04065
hychothetical protein F28M11.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 02-Sep-2000
C:Accession: T04065
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 1999
A:Reference number: 215184
A:Accession: T04065
A:Molecule type: DNA
A:Residues: 1-236 <BEV>

```

A:Cross-references: EMBL:AL049487
A:Experimental source: cultivar Columbia; BAC clone F28M11
C:Genetics:
A:Map position: 4
A:Introns: 82/3; 110/2
A:Note: F28M11.70
C:Superfamily: RING finger homology
E:107-158/Domain: RING finger homology <RNN>

Query Match	29.5%	Score 84.5	DB 2	Length 236
Best Local Similarity	31.2%	Pred. NO. 0.0061		
Matches 15; Conservative	9;	Mismatches 21;	Indels 3;	Gaps 2
QY	4	CTTCSDFFDHSRDVAM--DCGHTFFHLCLIOSEFAPSRPTCQCQRIQY	50	
Db	111	CSVCLGDIYQAEKLDQMPSCGHTFFMECT--DLMTSTHTTCLYCRSL	156	

```
Search completed: September 4, 2002, 16:13:06
Job time: 3250 sec
```

```
QY      4 CTICSEDFDHSRDVAAM-DCGTFHLOCLIQSFETAPSRFCPOCRIQ 50
      1::: | | | | |::: | | | | |:::
Db     111 CSVCLGDYQAEKLIQMPSCGTFHMECI--DLMLTSHHTCPICRLSL 156
```

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